

***Bartonella* spp. and Typhus Group Rickettsiae among Persons Experiencing Homelessness, São Paulo, Brazil**

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Persons experiencing homelessness in São Paulo, Brazil, were seropositive for *Bartonella* spp. (79/109, 72.5%) and typhus group rickettsiae (40/109, 36.7%). *Bartonella quintana* DNA was detected in 17.1% (14/82) body louse pools and 0.9% (1/114) blood samples. Clinicians should consider vectorborne agents as potential causes of febrile syndromes in this population.

Persons experiencing homelessness might be predisposed to vectorborne infections because of increased exposure to ectoparasites (1). Members of the genera *Bartonella* and *Rickettsia*, particularly the louseborne pathogens *B. quintana* and *R. prowazekii*, are agents of emerging illnesses among persons who are marginalized or experiencing homelessness (1). Studies on *Bartonella* and *Rickettsia* spp. infections in homeless populations within Latin America are scarce (2,3). Infestations with *Pediculus humanus humanus* body lice were reported in persons

experiencing homelessness in Curitiba and São Paulo, 2 major cities in Brazil (4). We report results of molecular testing of lice and blood from persons experiencing homelessness in the city of São Paulo in southeastern Brazil. We evaluated their possible exposure to *Bartonella* spp. and typhus group rickettsiae (TGR) by using indirect immunofluorescence assays (IFAs). In addition, we assessed risk factors related to serologic status.

The Study

During June–August 2018, a total of 114 persons experiencing homelessness (101 men, 13 women; average age 42.5 ±13.4 years) from a day-shelter in the city of São Paulo signed written informed consent forms and participated in this study, which was approved by the National Ethics Committee in Human Research (protocol no. 80099017.3.0000.0102). Persons responded to a questionnaire that, combined with medical and demographic records (Appendix, <https://wwwnc.cdc.gov/EID/article/29/2/22-1050-App1.pdf>), we used to assess risk factors. We carefully examined personal clothing and found lice in 14.9% (17/114, 95% CI 6.9%–19.7%) of persons; the lice were taxonomically identified as *P. humanus humanus* (5).

We analyzed 109 serum samples from study participants by using IFA to detect IgG against *Bartonella* spp. and TGR. We used commercial slides for *B. quintana* (12-well IFA Substrate Slides; Fuller Laboratories, <http://www.fullerlaboratories.com>) and in-house slides for *B. henselae* sequence type 9, *B. macedoniae* 56A, *R. typhi* Galveston, and *R. prowazekii* Breinl strains. We found 79/109 (72.5%, 95% CI 63.1%–80.1%) persons were seropositive for *Bartonella* spp. and 40/109 (36.7%, 95% CI 27.7%–46.5%) were sero-

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positive for TGR (titers ≥ 64). All antibody titers were ≥ 128 (Appendix Table 1), except for 2 *B. quintana*-positive and 8 TGR-positive samples. An endpoint titer ≥ 4 -fold higher for a particular *Bartonella*/*Rickettsia* spp. antigen than that observed for other *Bartonella*/*Rickettsia* spp. antigens was considered the possible antigen involved in a homologous reaction (PAIHR) (6). Thus, *B. quintana* was the PAIHR in 75/79 (95.0%, 95% CI 87.5%–98.6%) persons, *R. typhi* was the PAIHR in 13/40 (32.5%, 95% CI 18.6%–49.1%) persons, and *R. prowazekii* was the PAIHR in 3/40 (7.5%, 95% CI 1.6%–20.4%) persons (Appendix Table 1).

We extracted DNA by using the Blood/Tissue DNA Kit (MEBEP Bio Science, <https://www.mebep.com>) for 114 blood samples and guanidine isothiocyanate and phenol/chloroform technique (7) for 638 lice (82 pools). We confirmed successful extractions by PCR of glyceraldehyde-3-phosphate dehydrogenase (blood) and invertebrate mitochondrial cytochrome c oxidase subunit I (lice) genes (8,9). We screened DNA samples for *Bartonella* spp. by PCR of citrate synthase (*gltA*) and β subunit of RNA polymerase (*rpoB*) genes and for *Rickettsia* spp. by PCR of rickettsial 17-kDa antigen gene, as previously described (10–12). We used ultrapure water as a negative control and genomic DNA from *B. henselae* and *R. sibirica* as positive controls. A total of 14/82 (17.0%, 95% CI 9.7%–27.0%) louse pools and 1/114 (0.9%, 95% CI 0.02%–4.8%) blood samples were positive for *gltA* and *rpoB* but negative for *Rickettsia* spp. (Appendix Table 2).

Amplicons were purified and sequenced at the University of Texas Medical Branch (Galveston, TX, USA). The *gltA* and *rpoB* sequences showed 100% identity to *B. quintana* strain NCTC12899 (GenBank accession no. LS483373.1) by BLASTn analysis (<https://blast.ncbi.nlm.nih.gov>). *B. quintana* sequences generated in this study were deposited in GenBank (accession nos. ON808843 and ON808844). The person whose blood was PCR-positive for *B. quintana* was not infested with body lice but demonstrated high levels of IgG against *B. quintana* (titer $\geq 1,024$) and TGR (titers were 1,024 for *R. typhi* and 512 for *R. prowazekii*).

We chose risk factor variables by using unconditional logistic regression models ($p < 0.25$) and conditional logistic regression to determine relationships between putative risk factors and serologic status. We used Bayesian information criteria to assess the goodness-of-fit for the models. We used R software version 4.1.2 (The R Project for Statistical Computing, <https://www.r-project.org>) for all statistical analyses and summarized the final conditional logistic regression model (Table). Although the final model for *Bartonella* spp. revealed 3 variables, only 1 was statistically

significant and showed an association between body louse infestation and higher risk for *Bartonella* spp. seropositivity (OR [odds ratio] 2.9, 90% CI 1.1–8.1). The final TGR model contained 5 variables of which 3 were associated with higher seropositivity risk, including self-identifying as white (OR 3.9, 90% CI 1.6–10.7), syphilis seropositivity (OR 3.6, 90% CI 1.5–9.4), and homelessness because of unemployment (OR 2.3, 90% CI 1.02–5.5). We detected 5 variables for combined *Bartonella* spp. and TGR of which 4 variables were associated with seropositivity, including self-identifying as white (OR 5.6, 90% CI 2.2–15.5), monthly change of clothes (OR 0.08, 90% CI 0.07–0.4), homelessness because of family conflicts (OR 0.4, 90% CI 0.2–0.8), and higher total plasma protein (OR 2.0, 90% CI 1.1–4.0).

Conclusions

Our study revealed *Bartonella* spp. and TGR exposure, associated risk factors related to serologic status, and *B. quintana* detection in lice and one blood sample among persons experiencing homelessness in São Paulo, Brazil. Seroprevalence of *Bartonella* spp. (72.5%) was higher in our study than previous reports for persons experiencing homelessness (1.8%–65%) (13), and *B. quintana* was the dominant antigen involved in homologous reactions. The highest *B. quintana* seroprevalence was previously found in France (65%, antibody titers ≥ 100) and Japan (57%, titers ≥ 128) (13); those titers were considered indicative of previous exposure. In our study, the antibody titer cutoff was ≥ 64 , explaining our high seroprevalence results, although all but 2 titers were ≥ 128 . TGR seropositivity in our study (36.7%) was within the range observed in the United States, Europe, and Colombia (0.54%–56.2%) (1,3).

Persons experiencing homelessness in São Paulo had *P. humanus humanus* body louse infestation and seropositivity for *B. quintana* and TGR similar to that reported previously (1). Body louse infestation (14.9%) was within the range of other reports (7%–22%) (14), highlighting global vulnerability to louse infestation and louseborne diseases in persons experiencing homelessness (1).

Through logistic regression, we showed seropositivity for *Bartonella* spp. was associated with louse infestation. Because the association of white ethnicity and TRG seropositivity (alone and in combination with *Bartonella* spp.) might be from a skewed population sampling, our findings should be further investigated. Nonetheless, higher TGR seropositivity was associated with homelessness because of unemployment, duration of homelessness, and syphilis seropositivity,

Table. Conditional logistic regression model results showing factors associated with exposure to *Bartonella* spp. and TGR among persons experiencing homelessness in São Paulo, Brazil, June–August 2018*

Model variables	Odds ratio (90% CI)	p value
<i>Bartonella</i> spp.†		
Intercept	1.72 (0.86–3.56)	0.20
Ethnicity		
Not white	Referent	NA
White	1.03 (0.30–5.40)	0.97
Body lice infestation		
No	Referent	NA
Yes	2.86 (1.06–8.06)	0.08
Have cats		
No	Referent	NA
Yes	0.24 (0.04–1.10)	0.13
TGR‡		
Intercept	0.47 (0.21–1.02)	0.11
Ethnicity		
Not white	Referent	NA
White	3.94 (1.56–10.67)	0.02
Cause of homelessness: unemployment		
No	Referent	NA
Yes	2.33 (1.02–5.46)	0.09
Frequency of changing clothes		
>Monthly	Referent	NA
Monthly	0.01 (0.001–99.53)	0.99
Syphilis infection		
No	Referent	NA
Yes	3.64 (1.50–9.37)	0.02
Duration of homelessness		
<1 y	Referent	NA
>1 y	0.65 (0.28–1.51)	0.40
Combined <i>Bartonella</i> spp. and TGR§		
Intercept	0.001 (0.0001–0.03)	0.02
Ethnicity		
Not white	Referent	NA
White	5.56 (2.18–15.50)	0.004
Total plasma protein	2.01 (1.04–4.00)	0.086
Packed cell volume	1.09 (0.99–1.21)	0.127
Cause of homelessness: family conflicts		
No	Referent	NA
Yes	0.36 (0.16–0.80)	0.038
Frequency of changing clothes		
>Monthly	Referent	NA
Monthly	0.08 (0.07–0.42)	0.03

*Bayesian information criteria (BICs) were used to assess the goodness-of-fit for each model. NA, not applicable; TGR, typhus group rickettsiae.

†Model BIC = 100.1.

‡Model BIC = 139.6.

§Model BIC = 140.5.

which represent risk factors that reflect vulnerability and socioeconomic conditions. In addition, seropositivity for both *Bartonella* and TGR was associated with infrequent changes of clothing.

The first limitation of our study is that the small sample size and power for the examined variables might have weakened associations of *Bartonella* seroreactivity with other variables included in our questionnaire, such as alcoholism, tobacco or intravenous drug use, and homelessness as previously reported (15), and variables that were significant in univariate analysis. In addition, IgG seropositivity reflects past *Bartonella* and TGR infections (6,13). IFA cross-reactivity should be addressed with future studies by using cross-adsorption techniques.

Our results should alert public health professionals in the city of São Paulo to initiate preemptive measures and active vector control among persons experiencing homelessness and confirm circulation of *Bartonella* and TGR species. Clinicians should also consider these vectorborne agents as probable etiologic agents of febrile syndromes in this vulnerable population.

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Appendix

Additional Methods

Persons experiencing homelessness responded to a questionnaire that, combined with medical and demographic records, was used to assess risk factors for exposure to *Bartonella* spp. and typhus group rickettsiae in São Paulo city, Brazil, during June–August 2018. The questionnaire was administered in the Brazilian Portuguese language and verbal responses were recorded by a project coordinator.

Questionnaire Information

Demographic variables

- Sample location (diverse locations within São Paulo city, Brazil)
- Neighborhood of sampling (diverse neighborhoods within São Paulo city, Brazil)
- Age (years)
- Sex or gender (male/female)
- Marital status (single/married)
- Self-identified race/ethnicity (white/not white)
- Education (illiterate/literate/not informed)
- Assistance by counselling and psychological services (yes/no)
- Current drug use (yes/no)
- Alcohol consumption (yes/no)
- Tobacco consumption (yes/no)

- Marijuana consumption (yes/no)
- Cocaine consumption (yes/no)
- Crack consumption (yes/no)
- Other drug consumption (drug name)
- City of origin (city in Brazil, city outside Brazil, other country)
- Travel to other cities (yes/no/no response)
- Homelessness duration (months)
- Resting place: shelter/friend's home (yes/no)
- Resting place: on the street (yes/no)
- Resting place: settlement (yes/no)
- Causes for homelessness (yes/no/not informed; following options: lost home; alcohol and drugs, unemployment, family conflicts)
- Has any companion animals? (yes/no/no response)
- Has dog as companion animal? (yes/no/no response)
- Number of dogs that he/she has (number)
- Has cat as companion animal? (yes/no/no response)
- Number of cats that he/she has (number)
- How many people do you live with? (0–2 persons/3–4 persons/>5 persons/no response)
- Frequency of showering (daily/2 times per week/weekly/monthly/no response)
- Do you launder your clothes? (yes/no)
- How do you launder your clothes? (yes/no/not informed; following options: with water, soap and water, soak clothes).
- Do you change your clothes? (daily/2 times per week/weekly/monthly/no response)
- Do you share clothes? (yes/no/no response)
- Do you know what body lice are? (yes/no/no response)

- Have you experienced a previous body louse infestation? (yes/no/no response/not evaluated)
- Have you seen rats? (yes/no/no response/not evaluated)
- Frequency of rat visualization (daily/1 time per week/>1 time per week/not seen/no response/not evaluated)
- Have you experienced a rat bite (yes/no/no response/not evaluated)
- Presence of body lice at the moment of sampling (yes/no)

Medical variables

- Chest pain (yes/no/no response)
- Joint pain (yes/no/no response)
- Eye pain (yes/no/no response)
- Headache (yes/no/no response)
- Difficulty breathing (yes/no/no response)
- Abdominal pain (yes/no/no response)
- Fever for ≥ 2 weeks with unknown origin (continuous/relapsing/no/no response/not evaluated)
- Autoimmune disease (yes/no/no response)
- Which autoimmune disease? (open response)
- Self-care appearance (yes/no/not evaluated)
- Unpleasant smell present (yes/no/not evaluated)
- Packed cell volume, data obtain from (1)
- Total protein, data obtain from (1).
- HIV serological status, data obtain from (2)
- Syphilis serological status, data obtain from (2)
- Hepatitis C serological status, data obtain from (2).

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Appendix Table 1. Titers of IgG against *Bartonella* and typhus group rickettsiae in 109 blood samples from persons experiencing homelessness in São Paulo, Brazil, during June–August 2018*

Sample†	<i>B. quintana</i>	<i>B. machadoae</i>	<i>B. henselae</i>	<i>R. typhi</i>	<i>R. prowazekii</i>	Interpretation
SP01	512	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP02	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP03	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP05	256	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP11	256	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP14	256	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP16	512	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP17	512	<64	<64	128	128	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP18	256	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP19	512	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP20	256	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP21	128	<64	<64	128	128	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP24	512	<64	<64	256	256	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP25	≥1024	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP26	≥1024	<64	<64	512	512	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP27	≥1024	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP28	≥1024	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP29	≥1024	<64	<64	512	512	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP30	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP31	256	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP33	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP34	512	<64	<64	128	128	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP35	256	64	64	<64	128	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i> and <i>R. prowazekii</i>
SP36	512	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP37	256	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP38	≥1024	64	<64	≥1024	≥1024	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP39	≥1024	<64	<64	512	512	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP40	256	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP41	≥1024	<64	<64	512	≥1024	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i> and <i>R. prowazekii</i>
SP42	256	<64	<64	128	128	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP43	64	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive
SP44	≥1024	64	64	128	64	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>

Sample†	<i>B. quintana</i>	<i>B. machadoae</i>	<i>B. henselae</i>	<i>R. typhi</i>	<i>R. prowazekii</i>	Interpretation
SP45	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP46	≥1024	<64	<64	512	256	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP47	≥1024	64	64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP48	128	64	64	<64	<64	<i>Bartonella</i> spp. seroreactive
SP49	128	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP50	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP51	≥1024	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP52	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP53	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP54	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP55	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP56	≥1024	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP57	≥1024	<64	<64	256	64	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i> and <i>R. typhi</i>
SP58	<64	<64	<64	64	<64	TGR seroreactive
SP59	<64	<64	<64	64	<64	TGR seroreactive
SP60	<64	<64	64	64	<64	<i>Bartonella</i> and TGR seroreactive
SP61	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP62	512	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP63	512	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP64	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP65	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP66	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP67	≥1024	<64	<64	≥1024	512	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i> and <i>R. typhi</i>
SP68	≥1024	64	64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP69	512	64	256	256	256	<i>Bartonella</i> and TGR seroreactive
SP70	≥1024	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP71	512	<64	<64	≥1024	256	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i> and <i>R. typhi</i>
SP72	≥1024	<64	<64	512	128	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i> and <i>R. typhi</i>
SP73	512	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP74	<64	<64	<64	<64	128	TGR seroreactive; PAIHR, <i>R. prowazekii</i>
SP75	≥1024	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP76	128	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP77	256	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP78	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP79	512	<64	<64	256	64	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i> and <i>R. typhi</i>
SP80	≥1024	64	64	64	<64	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP81	256	<64	<64	64	64	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP82	512	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP83	≥1024	<64	<64	128	128	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP84	64	<64	<64	<64	<64	<i>Bartonella</i> sp. seroreactive
SP85	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP86	<64	<64	<64	<64	64	TGR seroreactive
SP87	≥1024	<64	<64	256	128	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP88	≥1024	<64	<64	256	64	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i> and <i>R. typhi</i>
SP89	512	<64	<64	≥1024	512	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i> and <i>R. typhi</i>
SP90	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP91	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP92	≥1024	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP93	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP94	512	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP95	256	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP96	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP97	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP99	≥1024	<64	<64	≥1024	512	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i> and <i>R. typhi</i>
SP100	512	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP101	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR

Sample†	<i>B. quintana</i>	<i>B. machadoae</i>	<i>B. henselae</i>	<i>R. typhi</i>	<i>R. prowazekii</i>	Interpretation
SP102	256	<64	64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP103	≥1024	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP104	256	64	<64	≥1024	512	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i> and <i>R. typhi</i>
SP105	256	<64	<64	<64	64	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP106	256	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP107	≥1024	<64	<64	≥1024	512	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i> and <i>R. typhi</i>
SP108	≥1024	<64	<64	64	64	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP109	512	<64	<64	256	64	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i> and <i>R. typhi</i>
SP110	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP111	128	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP112	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP113	≥1024	<64	64	256	64	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i> and <i>R. typhi</i>
SP114	256	<64	<64	<64	<64	<i>Bartonella</i> spp. seroreactive; PAIHR, <i>B. quintana</i>
SP115	≥1024	<64	<64	128	64	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP 116	≥1024	64	<64	256	128	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP118	≥1024	<64	<64	128	64	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP119	<64	<64	<64	256	<64	TGR seroreactive; PAIHR, <i>R. typhi</i>
SP120	512	<64	<64	512	256	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP121	<64	<64	<64	<64	<64	Not seroreactive to <i>Bartonella</i> spp. or TGR
SP122	512	<64	<64	128	64	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>
SP123	≥1024	<64	<64	512	256	<i>Bartonella</i> and TGR seroreactive; PAIHR, <i>B. quintana</i>

*IgG titers were determined by indirect immunofluorescence assay with commercial slides for *Bartonella quintana* (12-well IFA Substrate Slides, Fuller Laboratories, <http://www.fullerlaboratories.com>) and in-house slides for *B. henselae* ST9, *B. machadoae* 56A, *Rickettsia typhi* Galveston, and *Rickettsia prowazekii* Breinl strains. PAIHR, possible antigen involved in a homologous reaction; TGR, typhus group rickettsiae.

†Serum samples were not available for SP07, SP22, and SP32.

Appendix Table 2. Detection of *Bartonella* and *Rickettsia* spp. DNA in lice collected from persons (n = 17) experiencing homelessness in São Paulo, Brazil, during June–August 2018*

Sample ID*	Body louse pool ID	Composition of body louse pools	<i>Bartonella</i> spp./ <i>Rickettsia</i> spp. DNA
SP01	2	4 males	Negative/Negative
	3	10 nymphs	Negative/Negative
	4	8 nymphs	Negative/Negative
SP07	6	1 female	Negative/Negative
	7	10 nymphs	Negative/Negative
	8	10 nymphs	Negative/Negative
	9	10 nymphs	Negative/Negative
	10	10 nymphs	Negative/Negative
	11	8 nymphs	Negative/Negative
SP19	No DNA extraction		NA
SP22	13	1 male	Negative/Negative
	15	1 nymph	Negative/Negative
SP26	16	1 male	Negative/Negative
SP27	18	6 males	Negative/Negative
	19	6 males	Negative/Negative
	21	6 females	Negative/Negative
	22	10 nymphs	Negative/Negative
	23	10 nymphs	Negative/Negative
	24	10 nymphs	Negative/Negative
	25	10 nymphs	Negative/Negative
	26	10 nymphs	Negative/Negative
	27	10 nymphs	Negative/Negative
	29	10 nymphs	Negative/Negative
	30	10 nymphs	Negative/Negative
	31	10 nymphs	Negative/Negative
	32	10 nymphs	Negative/Negative

Sample ID*	Body louse pool ID	Composition of body louse pools	<i>Bartonella</i> spp./ <i>Rickettsia</i> spp. DNA
	33	10 nymphs	Negative/Negative
	34	10 nymphs	Negative/Negative
	35	10 nymphs	Negative/Negative
	36	10 nymphs	Negative/Negative
	37	10 nymphs	Negative/Negative
	38	10 nymphs	Negative/Negative
	39	10 nymphs	Negative/Negative
	40	10 nymphs	Negative/Negative
	41	10 nymphs	Negative/Negative
	42	10 nymphs	Negative/Negative
	43	10 nymphs	Negative/Negative
	44	10 nymphs	Negative/Negative
	45	10 nymphs	Negative/Negative
	46	10 nymphs	Negative/Negative
	47	10 nymphs	Negative/Negative
	48	10 nymphs	Negative/Negative
	49	10 nymphs	Negative/Negative
	50	10 nymphs	Negative/Negative
	51	10 nymphs	Negative/Negative
	52	10 nymphs	Negative/Negative
	53	10 nymphs	Negative/Negative
	54	10 nymphs	Negative/Negative
	56	10 nymphs	Negative/Negative
SP31	58	6 nymphs	Negative/Negative
SP32	60	4 females	Negative/Negative
	61	6 nymphs	Negative/Negative
SP47	No DNA extraction	NA	NA
SP65	65	2 males	Negative/Negative
	67	6 nymphs	Negative/Negative
	68	5 nymphs	Negative/Negative
SP75	No DNA extraction	NA	NA
SP79	No DNA extraction	NA	NA
SP80	71	5 males	Positive/Negative
	72	5 males	Positive/Negative
	73	5 males	Negative/Negative
	74	5 males	Positive/Negative
	75	5 males	Positive/Negative
	76	5 males	Negative/Negative
	77	5 males	Positive/Negative
	79	5 males	Positive/Negative
	80	4 males	Positive/Negative
	83	5 females	Positive/Negative
	84	5 females	Positive/Negative
	85	5 females	Positive/Negative
	86	5 females	Positive/Negative
	87	5 females	Positive/Negative
	88	5 females	Negative/Negative
	89	5 females	Positive/Negative
	90	5 females	Negative/Negative
	91	3 females	Negative/Negative
	93	10 nymphs	Negative/Negative
	94	10 nymphs	Negative/Negative
	96	10 nymphs	Negative/Negative
	97	10 nymphs	Negative/Negative
	98	10 nymphs	Negative/Negative
	99	10 nymphs	Negative/Negative
	100	10 nymphs	Negative/Negative
	101	10 nymphs	Negative/Negative
	102	10 nymphs	Negative/Negative
	103	10 nymphs	Positive/Negative
SP101	No DNA extraction	NA	NA
SP108	No DNA extraction	NA	NA
SP109	No DNA extraction	NA	NA
SP113	No DNA extraction	NA	NA

*We screened DNA samples for *Bartonella* spp. by PCR of citrate synthase (*gltA*) and β subunit of RNA polymerase (*rpoB*) genes and for *Rickettsia* spp. by PCR of rickettsial 17-kDa antigen gene. Results for antibodies against *Bartonella* and typhus group rickettsiae are in Appendix Table 1. ID, identification; NA, not applicable.